
Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 20 16:11:22 EDT 2007

Validated By CRFValidator v 1.0.3

Application No: 10518072 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-10 15:56:40.626

Finished: 2007-09-10 15:56:48.761

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms

Total Warnings: 103

Total Errors: 121

No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Err	or code	Error Description
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
W	402	Undefined organism found in <213> in SEQ ID (4)
W	402	Undefined organism found in <213> in SEQ ID (5)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (5)

Output Set:

Started: 2007-09-10 15:56:40.626 **Finished:** 2007-09-10 15:56:48.761

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 135 ms

Total Warnings: 103

Total Errors: 121

No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Err	or code	Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W	402	Undefined organism found in <213> in SEQ ID (6)
W	402	Undefined organism found in <213> in SEQ ID (7)
W	402	Undefined organism found in <213> in SEQ ID (13)
W	402	Undefined organism found in <213> in SEQ ID (14)
W	402	Undefined organism found in <213> in SEQ ID (16)
W	402	Undefined organism found in <213> in SEQ ID (18)
W	402	Undefined organism found in <213> in SEQ ID (21)
W	402	Undefined organism found in <213> in SEQ ID (23)
W	402	Undefined organism found in <213> in SEQ ID (24)
W	402	Undefined organism found in <213> in SEQ ID (25)
W	402	Undefined organism found in <213> in SEQ ID (30)
W	402	Undefined organism found in <213> in SEQ ID (31)
W	402	Undefined organism found in <213> in SEQ ID (33)
W	402	Undefined organism found in <213> in SEQ ID (35)
W	402	Undefined organism found in <213> in SEQ ID (38)
W	213	Artificial or Unknown found in <213> in SEQ ID (39)
W	213	Artificial or Unknown found in <213> in SEQ ID (40)
W	213	Artificial or Unknown found in <213> in SEQ ID (41)
W	213	Artificial or Unknown found in <213> in SEQ ID (42)
W	213	Artificial or Unknown found in <213> in SEQ ID (43)

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Total Warnings: 103

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No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Err	or code	Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (44)
W	213	Artificial or Unknown found in <213> in SEQ ID (45)
W	213	Artificial or Unknown found in <213> in SEQ ID (46)
W	213	Artificial or Unknown found in <213> in SEQ ID (47)
W	213	Artificial or Unknown found in <213> in SEQ ID (48)
W	213	Artificial or Unknown found in <213> in SEQ ID (49)
W	213	Artificial or Unknown found in <213> in SEQ ID (50)
W	213	Artificial or Unknown found in <213> in SEQ ID (54)
W	213	Artificial or Unknown found in <213> in SEQ ID (55)
W	402	Undefined organism found in <213> in SEQ ID (56)
W	402	Undefined organism found in <213> in SEQ ID (57)
W	213	Artificial or Unknown found in <213> in SEQ ID (58)
W	213	Artificial or Unknown found in <213> in SEQ ID (59)
W	402	Undefined organism found in $<213>$ in SEQ ID (60) This error has occured more than 20 times, will not be displayed
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (63)
E	300	Invalid codon found Phe SEQID (63) POS: 432
E	300	Invalid codon found Leu SEQID (63) POS: 435
E	300	Invalid codon found Phe SEQID (63) POS: 438
E	300	Invalid codon found Leu SEQID (63) POS: 441
E	300	Invalid codon found Gly SEQID (63) POS: 444
E	300	Invalid codon found Thr SEQID (63) POS: 447

Output Set:

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Total Warnings: 103

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No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Err	or code	Error Description
E	300	Invalid codon found Pro SEQID (63) POS: 450
E	300	Invalid codon found Glu SEQID (63) POS: 453
E	300	Invalid codon found Ala SEQID (63) POS: 456
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (64)
E	300	Invalid codon found Pro SEQID (64) POS: 289
E	300	Invalid codon found Lys SEQID (64) POS: 292
E	300	Invalid codon found Asn SEQID (64) POS: 295
E	300	Invalid codon found Ala SEQID (64) POS: 298
E	300	Invalid codon found Ala SEQID (64) POS: 301
E	300	Invalid codon found Val SEQID (64) POS: 304
E	300	Invalid codon found Met SEQID (64) POS: 307
E	300	Invalid codon found Leu SEQID (64) POS: 310
E	300	Invalid codon found Trp SEQID (64) POS: 313
E	300	Invalid codon found Ile SEQID (64) POS: 316
E	300	Invalid codon found Phe SEQID (64) POS: 319 This error has occured more than 20 times, will not be displayed
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed
E	355	Empty lines found between the amino acid numbering and the

Output Set:

Started: 2007-09-10 15:56:40.626 **Finished:** 2007-09-10 15:56:48.761

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Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 129

Actual SeqID Count: 129

Err	or code	Error Description
E	321	No. of Bases conflict, this line has no nucleotides SEQID (78)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (83)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (97)
W	213	Artificial or Unknown found in <213> in SEQ ID (123)
W	213	Artificial or Unknown found in <213> in SEQ ID (124)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (125)
W	213	Artificial or Unknown found in <213> in SEQ ID (128)
W	213	Artificial or Unknown found in <213> in SEQ ID (129) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING <110> Weill, Mylene Fort, Philippe Raymond, Michel Pasteur, Nicole <120> NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF <130> 263365US0XPCT <140> 10518072 <141> 2007-09-10 <150> FR 02/07622 <151> 2002-06-20 <150> FR 02/13799 <151> 2002-11-05 <160> 129 <170> PatentIn version 2.1 <210> 1 <211> 524 <212> PRT <213> Anopheles gambiae <400> 1 Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile Pro 20 25 Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg Pro 35 40 Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Thr Pro Pro Asn Ser 50 55 Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr 70 75 65

Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
100 105 110

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn

Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr 115 120 125

Asp	His 130	Arg	Ala	Leu	Ala	Ser 135	Glu	Glu	Asn	Val	Ile 140	Val	Val	Ser	Leu
Gln 145	Tyr	Arg	Val	Ala	Ser 150	Leu	Gly	Phe	Leu	Phe 155	Leu	Gly	Thr	Pro	Glu 160
Ala	Pro	Gly	Asn	Ala 165	Gly	Leu	Phe	Asp	Gln 170	Asn	Leu	Ala	Leu	Arg 175	Trp
Val	Arg	Asp	Asn 180	Ile	His	Arg	Phe	Gly 185	Gly	Asp	Pro	Ser	Arg 190	Val	Thr
Leu	Phe	Gly 195	Glu	Ser	Ala	Gly	Ala 200	Val	Ser	Val	Ser	Leu 205	His	Leu	Leu
Ser	Ala 210	Leu	Ser	Arg	Asp	Leu 215	Phe	Gln	Arg	Ala	Ile 220	Leu	Gln	Ser	Gly
Ser 225	Pro	Thr	Ala	Pro	Trp 230	Ala	Leu	Val	Ser	Arg 235	Glu	Glu	Ala	Thr	Leu 240
Arg	Ala	Leu	Arg	Leu 245	Ala	Glu	Ala	Val	Gly 250	Суз	Pro	His	Glu	Pro 255	Ser
Lys	Leu	Ser	Asp 260	Ala	Val	Glu	Суз	Leu 265	Arg	Gly	Lys	Asp	Pro 270	His	Val
Leu	Val	Asn 275	Asn	Glu	Trp	Gly	Thr 280	Leu	Gly	Ile	Cys	Glu 285	Phe	Pro	Phe
Val	Pro 290	Val	Val	Asp	Gly	Ala 295	Phe	Leu	Asp	Glu	Thr 300	Pro	Gln	Arg	Ser
Leu 305	Ala	Ser	Gly	Arg		Lys	_	Thr	Glu	Ile 315	Leu	Thr	Gly	Ser	Asn 320
Thr	Glu	Glu	Gly	Tyr 325	Tyr	Phe	Ile	Ile	Tyr 330	Tyr	Leu	Thr	Glu	Leu 335	Leu
Arg	Lys	Glu	Glu 340	Gly	Val	Thr	Val	Thr 345	Arg	Glu	Glu	Phe	Leu 350	Gln	Ala
Val	Arg	Glu 355	Leu	Asn	Pro	Tyr	Val 360	Asn	Gly	Ala	Ala	Arg 365	Gln	Ala	Ile
Val	Phe 370	Glu	Tyr	Thr	Asp	Trp 375	Thr	Glu	Pro	Asp	Asn 380	Pro	Asn	Ser	Asn
Arg 385	Asp	Ala	Leu	Asp	Lys 390	Met	Val	Gly	Asp	Tyr 395	His	Phe	Thr	Cys	Asn 400
Val	Asn	Glu	Phe	Ala 405	Gln	Arg	Tyr	Ala	Glu 410	Glu	Gly	Asn	Asn	Val 415	Tyr
Met	Tyr	Leu	Tyr 420	Thr	His	Arg	Ser	Lys 425	Gly	Asn	Pro	Trp	Pro 430	Arg	Trp

Thr Gly Val		Gly As	p Glu 440	Ile	Asn	Tyr	Val	Phe 445	Gly	Glu	Pro	
Leu Asn Pro	Thr Leu	Gly Ty		Glu	Asp	Glu	Lys 460	Asp	Phe	Ser	Arg	
Lys Ile Met 465	Arg Tyr	Trp Se	r Asn	Phe	Ala	Lys 475	Thr	Gly	Asn	Pro	Asn 480	
Pro Asn Thr	Ala Ser 485	Ser Gl	u Phe	Pro	Glu 490	Trp	Pro	Lys	His	Thr 495	Ala	
His Gly Arc	His Tyr 500	Leu Gl	u Leu	Gly 505	Leu	Asn	Thr	Ser	Phe 510	Val	Gly	
Arg Gly Pro	-	Arg Gl	n Cys 520	Ala	Phe	Trp	Lys					
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<220> <221> CDS <222> (1)	(1932)											
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<400> 2 atg ttt gtg Met Phe Val									-			48
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atg ttt gtg Met Phe Val 1 aac att tca	Cys Cys 5 gac gca	Phe Ph	e Phe t aca	Leu cca	Ser 10 tat	Leu ata	Ser ggt	Phe cac	Gys	Gly 15 gag	Ser	
atg ttt gtg Met Phe Val 1 aac att tca	Cys Cys 5 gac gca Asp Ala 20 ata gat Ile Asp	Phe	e Phe t aca e Thr	cca Pro 25	Ser 10 tat Tyr	Leu ata Ile	Ser ggt Gly gag	Phe cac His	Cys ggt Gly 30	Gly 15 gag Glu	tcc Ser	
atg ttt gtg Met Phe Val 1 aac att tca Asn Ile Ser gta cga att Val Arg Ile	Cys Cys 5 gac gca Asp Ala 20 ata gat Ile Asp	ttt tt Phe Ph gcc ga Ala Gl cga cg Arg Ar	t aca e Thr g ttg u Leu 40 c ggc	cca Pro 25 ggc Gly	ser 10 tat Tyr acg Thr	Leu ata Ile ctc Leu agg	ggt Gly gag Glu	Phe cac His cat His 45	Cys ggt Gly 30 gtc Val	Gly 15 gag Glu cac His	tcc Ser agt Ser	96
atg ttt gtg Met Phe Val 1 aac att tca Asn Ile Ser gta cga att Val Arg Ile 35 gga gca acg Gly Ala Thr	Cys Cys 5 gac gca Asp Ala 20 ata gat Ile Asp ccg cgg Pro Arg	ttt tt Phe Ph gcc ga Ala Gl cga cg Arg Ar	t aca e Thr g ttg u Leu 40 c ggc g Gly 5	cca Pro 25 ggc Gly ctg Leu	tat Tyr acg Thr	ata Ile ctc Leu agg Arg	ggt Gly gag Glu cgc Arg 60	cac His cat His 45 gag Glu	ggt Gly 30 gtc Val tca ser	Gly 15 gag Glu cac His	tcc Ser agt Ser tcg Ser	96 144
atg ttt gtg Met Phe Val 1 aac att tca Asn Ile Ser gta cga att Val Arg Ile 35 gga gca acg Gly Ala Thr 50 gac gcg aac Asp Ala Asr	Cys Cys 5 gac gca Asp Ala 20 ata gat Ile Asp ccg cgg Pro Arg	Phe	t aca e Thr g ttg u Leu 40 c ggc g Gly 5 g ctg o Leu t gcg	cca Pro 25 ggc Gly ctg Leu gtg Val	tat Tyr acg Thr acg Thr	ata Ile ctc Leu agg Arg aac Asn 75	ggt Gly gag Glu cgc Arg 60 acg Thr	cac His cat His 45 gag Glu gat Asp	ggt Gly 30 gtc Val tca Ser aag Lys	Gly 15 gag Glu cac His aac Asn	tcc Ser agt Ser tcg Ser cgc Arg 80	96 144 192

100 105 110

_		ccg Pro 115		_	-	-	_					_		_		384
	_	ccc Pro		-	-		_			_					_	432
	_	ggc Gly			_			_		_		_			_	480
_	_	tac Tyr					_	_	_				_			528
_	-	atg Met	_												_	576
	_	gac Asp 195			-						_					624
		gtg Val	_	_	_		_		_	_	_			_		672
	ggc	acc	ccq	gaa	aca	ccq	qqc	aat	aca	aaa	cta	ttc	gat	cad	aac	720
Leu 225	Gly	Thr	_	-		_					_		-	_		
225 ctt	dcd _	Thr cta Leu	Pro	Glu	Ala 230 gtg	Pro	Gly	Asn aac	Ala	Gly 235 cac	Leu	Phe ttc	Asp	Gln	Asn 240 gat	768
225 ctt Leu ccg	gcg Ala	cta	Pro cgc Arg	Glu tgg Trp 245	Ala 230 gtg Val	Pro cgg Arg	Gly gac Asp	Asn aac Asn gag	Ala att Ile 250	Gly 235 cac His	Leu cgg Arg	Phe ttc Phe	Asp ggt Gly	Gln ggc Gly 255	Asn 240 gat Asp	768
ctt Leu ccg Pro	gcg Ala tcg Ser	cta Leu cgt	ege Arg gtg Val 260	tgg Trp 245 aca Thr	Ala 230 gtg Val ctg Leu	egg Arg ttc Phe	Gly gac Asp ggc Gly	aac Asn gag Glu 265	Ala att Ile 250 agt Ser	Gly 235 cac His gcc Ala	cgg Arg ggt Gly	Phe ttc Phe gcc Ala	Asp ggt Gly gtc Val 270	ggc Gly 255 tcg Ser	Asn 240 gat Asp gtg Val	
ctt Leu ccg Pro tcg Ser	gcg Ala tcg Ser ctg	cta Leu cgt Arg	cgc Arg gtg Val 260 ctg Leu	tgg Trp 245 aca Thr	Ala 230 gtg Val ctg Leu tcc ser	cgg Arg ttc Phe gcc Ala	Gly gac Asp ggc Gly ctt Leu 280 acg	Asn aac Asn gag Glu 265 tcc ser	Ala att Ile 250 agt Ser cgc Arg	Gly 235 cac His gcc Ala gat Asp	cgg Arg ggt Gly ctg Leu	ttc Phe gcc Ala ttc Phe 285	Asp ggt Gly gtc Val 270 cag Gln	ggc Gly 255 tcg Ser cgg Arg	Asn 240 gat Asp gtg Val gcc Ala	816
ctt Leu ccg Pro tcg Ser atc Ile	gcg Ala tcg Ser ctg Leu ctg Leu 290	cta Leu cgt Arg cat His 275	cgc Arg gtg Val 260 ctg Leu agc ser	tgg Trp 245 aca Thr ctg Leu	Ala 230 gtg Val ctg Leu tcc Ser tcg Ser	cgg Arg ttc Phe gcc Ala ccg Pro 295	gac Asp ggc Gly ctt Leu 280 acg Thr	aac Asn gag Glu 265 tcc Ser gca Ala	Ala att Ile 250 agt Ser cgc Arg ccg Pro	Gly 235 cac His gcc Ala gat Asp tgg Trp	cgg Arg ggt Gly ctg Leu gca Ala 300	ttc Phe gcc Ala ttc Phe 285 ttg Leu	ggt Gly gtc Val 270 cag Gln gta Val	ggc Gly 255 tcg Ser cgg Arg	Asn 240 gat Asp gtg Val gcc Ala cgc Arg	816

325 330 335

aag	gac	ccg	cac	gtg	ctg	gtc	aac	aac	gag	tgg	ggc	acg	ctc	ggc	att	1056
Lys	Asp	Pro	His	Val	Leu	Val	Asn	Asn	Glu	Trp	Gly	Thr	Leu	Gly	Ile	
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tgc	gag	ttc	ccg	ttc	gtg	ccg	gtg	gtc	gac	ggt	gcg	ttc	ctg	gac	gag	1104
Cys	Glu	Phe	Pro	Phe	Val	Pro	Val	Val	Asp	Gly	Ala	Phe	Leu	Asp	Glu	
		355					360					365				
acg	ccg	cag	cgt	tcg	ctc	gcc	agc	ggg	cgc	ttc	aag	aag	acg	gag	atc	1152
Thr	Pro	Gln	Arg	Ser	Leu	Ala	Ser	Gly	Arg	Phe	Lys	Lys	Thr	Glu	Ile	
	370					375					380					
ctc	acc	ggc	agc	aac	acg	gag	gag	ggc	tac	tac	ttc	atc	atc	tac	tac	1200
Leu	Thr	Gly	Ser	Asn	Thr	Glu	Glu	Gly	Tyr	Tyr	Phe	Ile	Ile	Tyr	Tyr	
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ctg	acc	gag	ctg	ctg	cgc	aag	gag	gag	ggc	gtg	acc	gtg	acg	cgc	gag	1248
Leu	Thr	Glu	Leu	Leu	Arg	Lys	Glu	Glu	Gly	Val	Thr	Val	Thr	Arg	Glu	
				405					410					415		
gag	ttc	ctg	cag	gcg	gtg	cgc	gag	ctc	aac	ccg	tac	gtg	aac	ggg	gcg	1296
Glu	Phe	Leu	Gln	Ala	Val	Arg	Glu	Leu	Asn	Pro	Tyr	Val	Asn	Gly	Ala	
			420					425					430			
gcc	cgg	cag	gcg	atc	gtg	ttc	gag	tac	acc	gac	tgg	acc	gag	ccg	gac	1344
Ala	Arg	Gln	Ala	Ile	Val	Phe	Glu	Tyr	Thr	Asp	Trp	Thr	Glu	Pro	Asp	
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aac	ccg	aac	agc	aac	cgg	gac	gcg	ctg	gac	aag	atg	gtg	ggc	gac	tat	1392
	_		_			gac Asp		_	_	_	_			_		1392
	_		_			_		_	_	_	_			_		1392
	Pro		_			Asp		_	_	_	Met			_		1392
Asn	Pro 450	Asn	Ser	Asn	Arg	Asp	Ala	Leu	Asp	Lys	Met 460	Val	Gly	Asp	Tyr	1392 1440
Asn cac	Pro 450	Asn acc	Ser	Asn aac	Arg	Asp 455	Ala	Leu	Asp	Lys	Met 460 cgg	Val	Gly	Asp gag	Tyr gag	
Asn cac	Pro 450	Asn acc	Ser	Asn aac	Arg	Asp 455 aac	Ala	Leu	Asp	Lys	Met 460 cgg	Val	Gly	Asp gag	Tyr gag	
Asn cac His	Pro 450	Asn acc	Ser	Asn aac	Arg gtg Val	Asp 455 aac	Ala	Leu	Asp	Lys cag Gln	Met 460 cgg	Val	Gly	Asp gag	Tyr gag Glu	
Asn cac His 465	Pro 450 ttc Phe	Asn acc Thr	Ser tgc Cys	Asn aac Asn	Arg gtg Val 470	Asp 455 aac	Ala gag Glu	Leu ttc Phe	Asp gcg Ala	Lys cag Gln 475	Met 460 cgg Arg	Val tac Tyr	Gly gcc Ala	Asp gag Glu	Tyr gag Glu 480	
Asn cac His 465	Pro 450 ttc Phe	Asn acc Thr	tgc Cys	Asn aac Asn tac Tyr	Arg gtg Val 470	Asp 455 aac Asn	Ala gag Glu	ttc Phe	Asp gcg Ala acg Thr	Lys cag Gln 475	Met 460 cgg Arg	Val tac Tyr	Gly gcc Ala	Asp gag Glu ggc Gly	Tyr gag Glu 480	1440
Asn cac His 465	Pro 450 ttc Phe	Asn acc Thr	tgc Cys	Asn aac Asn	Arg gtg Val 470	Asp 455 aac Asn	Ala gag Glu	ttc Phe	Asp gcg Ala	Lys cag Gln 475	Met 460 cgg Arg	Val tac Tyr	Gly gcc Ala	Asp gag Glu ggc	Tyr gag Glu 480	1440
Cac His 465 ggc Gly	Pro 450 ttc Phe aac Asn	acc Thr aac Asn	tgc Cys gtc Val	Asn aac Asn tac Tyr 485	Arg gtg Val 470 atg	Asp 455 aac Asn tat Tyr	Ala gag Glu ctg Leu	ttc Phe tac Tyr	Asp gcg Ala acg Thr 490	Lys cag Gln 475 cac	Met 460 cgg Arg	Val tac Tyr agc Ser	Gly gcc Ala aaa Lys	Asp gag Glu ggc Gly 495	Tyr gag Glu 480 aac Asn	1440
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cac His 465 ggc Gly	Pro 450 ttc Phe aac Asn	Asn acc Thr aac Asn	tgc Cys gtc Val	aac Asn tac Tyr 485	gtg Val 470 atg Met	Asp 455 aac Asn tat Tyr	Ala gag Glu ctg Leu	ttc Phe tac Tyr	Asp gcg Ala acg Thr 490	cag Gln 475 cac His	Met 460 cgg Arg cgc Arg	Val tac Tyr agc ser	Gly gcc Ala aaa Lys atc Ile	Asp gag Glu ggc Gly 495	gag Glu 480 aac Asn	1440
cac His 465 ggc Gly	Pro 450 ttc Phe aac Asn	Asn acc Thr aac Asn	tgc Cys gtc Val	aac Asn tac Tyr 485	gtg Val 470 atg Met	Asp 455 aac Asn tat Tyr	Ala gag Glu ctg Leu	ttc Phe tac Tyr	Asp gcg Ala acg Thr 490	cag Gln 475 cac His	Met 460 cgg Arg cgc Arg	Val tac Tyr agc ser	Gly gcc Ala aaa Lys	Asp gag Glu ggc Gly 495	gag Glu 480 aac Asn	1440
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_	tcc Ser		_						_		_	_	-			1776
_	aag Lys				_		_	-	-		_				222	1824
	gca Ala 610	_		_	_	_	_	_	_	_	_				_	1872
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130 135 140

Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp 150 155 Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala 165 170 Ala Val Met Leu Trp Ile Phe Gly Gly Gly Phe Tyr Ser Gly Thr Ala 185 Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val 195 200 Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe 210 215 Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn 230 235 Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp 245 250 Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val 265 Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala 275 280 285 Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg 290 295 300 Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys 305 310 315 Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly 325 330 335 Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile 340 345 350 Cys Glu Phe Pro Phe Val Pro Val Asp Gly Ala Phe Leu Asp Glu 360 355 Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile 370 375 Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr 390 395 Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu 405 410 Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala 420 425

Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp 435 440 445

Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr 450 455 460

His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu 465 470 470 480

Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn \$485\$

Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr 500 505 510

 $\label{thm:conditional} \mbox{Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp G}$